quasi-purifying the specimen being assayed Hutchens et al. effectively overcame the primary limitation of MALDI mass spectrometry, namely, the suppression of ion signal due to overloading the matrix. They named their technique "surface-enhanced affinity capture mass spectrometry (SEAC)". They further demonstrated their technique by using single stranded DNA which they immobilized on the mass spectrometer probe tip to quasi-isolate the protein lactoferrin from preterm infant urine.—

C1 cont

Please replace the paragraph starting on page 5, line 17, with the following paragraph:

--The present invention combines and exploits the specificity of antibody-antigen binding and the ability of the mass spectrometer to unequivocally identify molecules in various qualitative and quantitative strategies to analyze one or more antigens or antibodies in a specimen within the limit of detection. Both qualitative and quantitative strategies utilize an antibody or antigen to capture and isolate another antigen or antibody, respectively, from its surroundings and thereafter mass spectrometrically analyze the isolated antibody or antigen after release from the capturing agent. This specificity of the antibody-antigen reaction coupled with the ability of the mass spectrometer to separate and unequivocally identify the captured and isolated antibody or antigen by its mass-to-charge ration from other molecules that may accompany it lends two dimensions of specificity to the present invention.--

C2

Please replace the paragraph starting on page 6, line 18, with the following paragraph:

--An article by Nelson, R., et al., published in Analytical Chemistry, vol. 67, pp 1153-1158, on or about March 31, 1995, describes certain portions of the present invention in detail.—

C3

Please replace the paragraph starting on page 17, line 9, with the following paragraph:

--**"Solid substrate"** is defined as any physically separable solid to which an antibody or antigen can be directly or indirectly attached including but not limited to agarose beads, nylon, metals, glass, silicon, and organic membranes.—

Please replace the paragraph starting on page 36, line 15, with the following paragraph:

--The analyte/IRS signal ratios in the addition-present mass spectral signals are then used to determine the analyte concentration in the addition-absent sample exactly as in the parallel standard addition approach. Since mass spectrometric immunoassay of each addition-present sample serves to calibrate a sample in which the concentration of the analyte differs from the analyte concentration in the addition-free sample by an amount which depends on the amounts of analyte captured in the preceding mass spectrometric immunoassays, it is apparent that the accuracy of this procedure will only be acceptable if the amount of analyte captured in each successive step is small, for example if 5% of the analyte is captured in the mass spectrometric immunoassay of the addition-free sample and mass spectrometric immunoassay of a single addition-present sample is performed, the analyte concentration determined thereby would be in error by 5%.—

Please replace the paragraph starting at page 46, line 24, with the following paragraph:

--An analytical sample, known to contain 12.5 nM AlAG was mass spectrometrically immunoassayed under similar conditions for the preparations above. The resulting AlAG signal was within that represented on the 5-point working curve of **FIG. 9** and is shown at point **–O-** corresponding to an AlAG concentration of ~12.5 nM which verifies the accuracy of the working curve quantification method.—

In the Claims:

The Examiner has renumbered claims 48-61 presented in Applicants' preliminary